

SEQUENCE LISTING

<110> SHINTANI et al.

<120> MEDICINAL USE OF MIP-3a INHIBITOR AND METHOD OF SCREENING BRAIN/NERVE CELL PROTECTIVE AGENT

<130> 20039.0001USWO

<140> 10/547,532

<141> 2005-08-31

<150> PCT/JP2004/002774

<151> 2004-03-04

<150> JP 2003-056885

<151> 2003-03-04

<150> JP 2003-106247

<151> 2003-04-10

<160> 21

<170> PatentIn version 3.1

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cta ctc cac ctc tgc ggc gaa tca gaa gca gca agc aac ttt gac tgc	96
Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys	
-10 -5 -1 1 5	
tgt ctt gga tac aca gac cgt att ctt cat cct aaa ttt att gtg ggc	144
Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly	
10 15 20	
ttc aca cgg cag ctg gcc aat gaa ggc tgt gac atc aat gct atc atc	192
Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile	

25	30	35	
ttt cac aca aag aaa aag ttg tct gtg tgc gca aat cca aaa cag act	240		
Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr			
40	45	50	
tggttg aaa tat att gtg cgt ctc ctc agt aaa aaa gtc aag aac atg	288		
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Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly	
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Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile	
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Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr	
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Ala Tyr Leu Cys Ser Gln Ser Glu Ala Ala Ser Asn Phe Asp Cys Cys	
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ctc acg tac aca aag aac gtg tat cat cat gcg aga aat ttt gtg ggt	144
Leu Thr Tyr Thr Lys Asn Val Tyr His His Ala Arg Asn Phe Val Gly	
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	20

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Phe	Thr	Thr	Gln	Met	Ala	Asp	Glu	Ala	Cys	Asp	Ile	Asn	Ala	Ile	Ile	
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Trp	Val	Lys	Arg	Ile	Leu	His	Leu	Leu	Ser	Leu	Arg	Thr	Lys	Lys	Met	
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Leu	Thr	Tyr	Thr	Lys	Asn	Val	Tyr	His	His	Ala	Arg	Asn	Phe	Val	Gly	
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Phe	Thr	Thr	Gln	Met	Ala	Asp	Glu	Ala	Cys	Asp	Ile	Asn	Ala	Ile	Ile	
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Phe	His	Leu	Lys	Ser	Lys	Arg	Ser	Val	Cys	Ala	Asp	Pro	Lys	Gln	Ile	
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Trp	Val	Lys	Arg	Ile	Leu	His	Leu	Leu	Ser	Leu	Arg	Thr	Lys	Lys	Met	
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Leu	Leu	Ala	His	Leu	Cys	Ser	Gln	Ala	Glu	Ala	Ala	Ser	Asn	Tyr	Asp	
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tgt	tgc	ctc	tcg	tac	ata	cag	acg	cct	ctt	cct	tcc	aga	gct	att	gtg	144

Cys	Cys	Leu	Ser	Tyr	Ile	Gln	Thr	Pro	Leu	Pro	Ser	Arg	Ala	Ile	Val		
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Gly	Phe	Thr	Arg	Gln	Met	Ala	Asp	Glu	Ala	Cys	Asp	Ile	Asn	Ala	Ile		
			25					30					35				
atc	ttt	cac	acg	aag	aaa	aga	aaa	tct	gtg	tgc	gct	gat	cca	aag	cag	240	
Ile	Phe	His	Thr	Lys	Lys	Arg	Lys	Ser	Val	Cys	Ala	Asp	Pro	Lys	Gln		
		40					45				50						
aac	tgg	gtg	aaa	agg	gct	gtg	aac	ctc	ctc	agc	cta	aga	gtc	aag	aag	288	
Asn	Trp	Val	Lys	Arg	Ala	Val	Asn	Leu	Leu	Ser	Leu	Arg	Val	Lys	Lys		
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	-10					-5				-1	1			5			
Cys	Cys	Leu	Ser	Tyr	Ile	Gln	Thr	Pro	Leu	Pro	Ser	Arg	Ala	Ile	Val		
			10					15					20				
Gly	Phe	Thr	Arg	Gln	Met	Ala	Asp	Glu	Ala	Cys	Asp	Ile	Asn	Ala	Ile		
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Ile	Phe	His	Thr	Lys	Lys	Arg	Lys	Ser	Val	Cys	Ala	Asp	Pro	Lys	Gln		
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Asn	Trp	Val	Lys	Arg	Ala	Val	Asn	Leu	Leu	Ser	Leu	Arg	Val	Lys	Lys		
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gat	tat	ttt	gtg	tca	gtc	aat	act	tca	tat	tac	tca	gtt	gat	tct	gag	96	
Asp	Tyr	Phe	Val	Ser	Val	Asn	Thr	Ser	Tyr	Tyr	Ser	Val	Asp	Ser	Glu		
		20					25					30					
atg	tta	ctg	tgc	tcc	ttg	cag	gag	gtc	agg	cag	ttc	tcc	agg	cta	ttt	144	
Met	Leu	Leu	Cys	Ser	Leu	Gln	Glu	Val	Arg	Gln	Phe	Ser	Arg	Leu	Phe		
	35					40				45							
gta	ccg	att	gcc	tac	tcc	ttg	atc	tgt	gtc	ttt	ggc	ctc	ctg	ggg	aat	192	
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	aca gac gtc tat ctc ttg aac atg gcc att gca gac atc ctc ttt gtt					288
	Thr Asp Val Tyr Leu Leu Asn Met Ala Ile Ala Asp Ile Leu Phe Val					
	85		90			95
	ctt act ctc cca ttc tgg gca gtg agt cat gcc act ggt gcg tgg gtt					336
	Leu Thr Leu Pro Phe Trp Ala Val Ser His Ala Thr Gly Ala Trp Val					
	100		105			110
	ttc agc aat gcc acg tgc aag ttg cta aaa ggc atc tat gcc atc aac					384
	Phe Ser Asn Ala Thr Cys Lys Leu Lys Gly Ile Tyr Ala Ile Asn					
	115		120			125
	ttt aac tgc ggg atg ctg ctc ctg act tgc att agc atg gac cgg tac					432
	Phe Asn Cys Gly Met Leu Leu Leu Thr Cys Ile Ser Met Asp Arg Tyr					
	130		135			140
	atc gcc att gta cag gcg act aag tca ttc cgg ctc cga tcc aga aca					480
	Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Leu Arg Ser Arg Thr					
	145		150			155
	cta ccg cgc agc aaa atc atc tgc ctt gtt gtg tgg ggg ctg tca gtc					528
	Leu Pro Arg Ser Lys Ile Ile Cys Leu Val Val Trp Gly Leu Ser Val					
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	atc atc tcc agc tca act ttt gtc ttc aac caa aaa tac aac acc caa					576
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	ggc agc gat gtc tgt gaa ccc aag tac cag act gtc tcg gag ccc atc					624
	Gly Ser Asp Val Cys Glu Pro Lys Tyr Gln Thr Val Ser Glu Pro Ile					
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	agg tgg aag ctg ctg atg ttg ggg ctt gag cta ctc ttt ggt ttc ttt					672
	Arg Trp Lys Leu Leu Met Leu Gly Leu Glu Leu Phe Gly Phe Phe					
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	Ile Pro Leu Met Phe Met Ile Phe Cys Tyr Thr Phe Ile Val Lys Thr					
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	Leu Val Gln Ala Gln Asn Ser Lys Arg His Lys Ala Ile Arg Val Ile					
	245		250			255
	ata gct gtg gtg ctt gtg ttt ctg gct tgt cag att cct cat aac atg					816
	Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro His Asn Met					
	260		265			270
	gtc ctg ctt gtg acg gct gca aat ttg ggt aaa atg aac cga tcc tgc					864
	Val Leu Leu Val Thr Ala Ala Asn Leu Gly Lys Met Asn Arg Ser Cys					
	275		280			285
	cag agc gaa aag cta att ggc tat acg aaa act gtc aca gaa gtc ctg					912
	Gln Ser Glu Lys Leu Ile Gly Tyr Thr Lys Thr Val Thr Glu Val Leu					
	290		295			300
	gct ttc ctg cac tgc tgc ctg aac cct gtg ctc tac gct ttt att ggg					960
	Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile Gly					
	305		310			315
	cag aag ttc aga aac tac ttt ctg aag atc ttg aag gac ctg tgg tgt					1008
	Gln Lys Phe Arg Asn Tyr Phe Leu Lys Ile Leu Lys Asp Leu Trp Cys					
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	gtg aga agg aag tac aag tcc tca ggc ttc tcc tgt gcc ggg agg tac					1056
	Val Arg Arg Lys Tyr Lys Ser Ser Gly Phe Ser Cys Ala Gly Arg Tyr					
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1122

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35 40 45
Val Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu Leu Gly Asn
50 55 60
Ile Leu Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser Met
65 70 75 80
Thr Asp Val Tyr Leu Leu Asn Met Ala Ile Ala Asp Ile Leu Phe Val
85 90 95
Leu Thr Leu Pro Phe Trp Ala Val Ser His Ala Thr Gly Ala Trp Val
100 105 110
Phe Ser Asn Ala Thr Cys Lys Leu Leu Lys Gly Ile Tyr Ala Ile Asn
115 120 125
Phe Asn Cys Gly Met Leu Leu Thr Cys Ile Ser Met Asp Arg Tyr
130 135 140
Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Leu Arg Ser Arg Thr
145 150 155 160
Leu Pro Arg Ser Lys Ile Ile Cys Leu Val Val Trp Gly Leu Ser Val
165 170 175
Ile Ile Ser Ser Ser Thr Phe Val Phe Asn Gln Lys Tyr Asn Thr Gln
180 185 190
Gly Ser Asp Val Cys Glu Pro Lys Tyr Gln Thr Val Ser Glu Pro Ile
195 200 205
Arg Trp Lys Leu Leu Met Leu Gly Leu Glu Leu Leu Phe Gly Phe Phe
210 215 220
Ile Pro Leu Met Phe Met Ile Phe Cys Tyr Thr Phe Ile Val Lys Thr
225 230 235 240
Leu Val Gln Ala Gln Asn Ser Lys Arg His Lys Ala Ile Arg Val Ile
245 250 255
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260 265 270
Val Leu Leu Val Thr Ala Ala Asn Leu Gly Lys Met Asn Arg Ser Cys
275 280 285
Gln Ser Glu Lys Leu Ile Gly Tyr Thr Lys Thr Val Thr Glu Val Leu
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Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile Gly
305 310 315 320
Gln Lys Phe Arg Asn Tyr Phe Leu Lys Ile Leu Lys Asp Leu Trp Cys
325 330 335
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 Glu Tyr Tyr Ser Ile Pro Pro Asp His Gly Pro Cys Ser Leu Glu Glu
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 Val Arg Asn Phe Thr Lys Val Phe Val Pro Ile Ala Tyr Ser Leu Ile
 35 40 45
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 Cys Val Phe Gly Leu Leu Gly Asn Ile Met Val Val Met Thr Phe Ala
 50 55 60
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 Phe Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met
 65 70 75 80
 gcc atc aca gac ata ctc ttt gtc ctc acc cta ccg ttc tgg gca gtt 288
 Ala Ile Thr Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val
 85 90 95
 act cat gcc acc aac act tgg gtt ttc agc gat gca ctg tgt aaa ctg 336
 Thr His Ala Thr Asn Thr Trp Val Phe Ser Asp Ala Leu Cys Lys Leu
 100 105 110
 atg aaa ggc aca tat gcg gtc aac ttt aac tgt ggg atg ctg ctc ctg 384
 Met Lys Gly Thr Tyr Ala Val Asn Phe Asn Cys Gly Met Leu Leu Leu
 115 120 125
 gcc tgt atc agc atg gac cgg tac att gcc atc gtc cag gca acc aaa 432
 Ala Cys Ile Ser Met Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys
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 Ser Phe Arg Val Arg Ser Arg Thr Leu Thr His Ser Lys Val Ile Cys
 145 150 155 160
 gtg gca gtg tgg ttc atc tcc atc atc atc tca agc cct aca ttt atc 528
 Val Ala Val Trp Phe Ile Ser Ile Ile Ile Ser Ser Pro Thr Phe Ile
 165 170 175
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 Phe Asn Lys Lys Tyr Glu Leu Gln Asp Arg Asp Val Cys Glu Pro Arg
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 Tyr Arg Ser Val Ser Glu Pro Ile Thr Trp Lys Leu Leu Gly Met Gly
 195 200 205
 ctg gag ctg ttc ttt ggg ttc ttc acc cct ttg ctg ttt atg gtg ttc 672
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Ala Cys Gln Ile Pro His Asn Met Val Leu Leu Val Thr Ala Val Asn							
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acg ggc aaa gtg ggc cgg agc tgc agc acc gag aaa gtc ctc gcc tac	864						
Thr Gly Lys Val Gly Arg Ser Cys Ser Thr Glu Lys Val Leu Ala Tyr							
		275		280		285	
acc agg aac gtg gcc gag gtc ctg gct ttc ctg cat tgc tgc ctc aac	912						
Thr Arg Asn Val Ala Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn							
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aag atc atg aag gat gtg tgg tgt atg aga agg aag aat aag atg cct	1008						
Lys Ile Met Lys Asp Val Trp Cys Met Arg Arg Lys Asn Lys Met Pro							
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Gly Phe Leu Cys Ala Arg Val Tyr Ser Glu Ser Tyr Ile Ser Arg Gln							
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 35 40 45
 Cys Val Phe Gly Leu Leu Gly Asn Ile Met Val Val Met Thr Phe Ala
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 Phe Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met
 65 70 75 80
 Ala Ile Thr Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val
 85 90 95
 Thr His Ala Thr Asn Thr Trp Val Phe Ser Asp Ala Leu Cys Lys Leu
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 Met Lys Gly Thr Tyr Ala Val Asn Phe Asn Cys Gly Met Leu Leu Leu
 115 120 125
 Ala Cys Ile Ser Met Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys
 130 135 140
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 145 150 155 160
 Val Ala Val Trp Phe Ile Ser Ile Ile Ile Ser Ser Pro Thr Phe Ile
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Lys Val Phe Val Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu	
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Leu Gly Asn Ile Met Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala	
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Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala Ile Thr Asp Ile	
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Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val Thr His Ala Thr Asp	
85 90 95 100	
act tgg atc ttt ggc aac acg atg tgt aaa ctg atg aaa ggc acg tat	690
Thr Trp Ile Phe Gly Asn Thr Met Cys Lys Leu Met Lys Gly Thr Tyr	
105 110 115	
gcg gtc aac ttt aac tgt ggg atg ctg ctc ctg gcc tgt atc agc atg	738
Ala Val Asn Phe Asn Cys Gly Met Leu Leu Leu Ala Cys Ile Ser Met	
120 125 130	
gac cgg tac att gcc atc gtc cag gcg acc aaa tct ttc cgg gta cgc	786
Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Val Arg	
135 140 145	
tcc aga aca ctg acg cac agt aag gtc atc tgt ctg acg gtg tgg ttc	834
Ser Arg Thr Leu Thr His Ser Lys Val Ile Cys Leu Thr Val Trp Phe	
150 155 160	
gtt tcc atc atc atc tca agc ccc aca ttc ttc ttc aac aag caa tac	882
Val Ser Ile Ile Ile Ser Ser Pro Thr Phe Phe Phe Asn Lys Gln Tyr	
165 170 175 180	
aag ctg cag ggc cgt gat gtc tgc gag cct cag tac aag ctc gtc tcg	930
Lys Leu Gln Gly Arg Asp Val Cys Glu Pro Gln Tyr Lys Leu Val Ser	
185 190 195	
gag ccc atc acg tgg aaa ctg ctg ggc atg gga ctc gag ctg ctc ttt	978
Glu Pro Ile Thr Trp Lys Leu Leu Gly Met Gly Leu Glu Leu Leu Phe	
200 205 210	
ggc ttc ttc atc cct ttg ctg ttt atg gtg ttc tgt tac ctg ttc atc	1026
Gly Phe Phe Ile Pro Leu Leu Phe Met Val Phe Cys Tyr Leu Phe Ile	
215 220 225	
atc aag acc ttg gtg cag gcc cag aat tcc aag agg cac aga gcc atc	1074
Ile Lys Thr Leu Val Gln Ala Gln Asn Ser Lys Arg His Arg Ala Ile	
230 235 240	
cga gtc gtg att gct gtg gtt ctc gtg ttc ctg gct tgt cag atc cct	1122
Arg Val Val Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro	

245		250		255		260	
cac aac atg gtc ctc ctc gtg act gca gcc aac acg ggc aaa atg ggc							1170
His Asn Met Val Leu Leu Val Thr Ala Ala Asn Thr Gly Lys Met Gly							
	265		270		275		
cgc agc tgc agc gcc gag aaa gcc ctc gcc tac gcc agg aat gtg gct							1218
Arg Ser Cys Ser Ala Glu Lys Ala Leu Ala Tyr Ala Arg Asn Val Ala							
	280		285		290		
gag gtc ctg gct ttc ctg cac tgc tgt ctc aac ccc gtg ttg tat gcc							1266
Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala							
	295		300		305		
ttc att gga cag aaa ttc aga agc tac ttc atg aag atc atg aag gat							1314
Phe Ile Gly Gln Lys Phe Arg Ser Tyr Phe Met Lys Ile Met Lys Asp							
	310		315		320		
gtg tgg tgt atg agg agg aag agc aag gtg cct acc ttc ttc tgt gcc							1362
Val Trp Cys Met Arg Arg Lys Ser Lys Val Pro Thr Phe Phe Cys Ala							
	325		330		335		340
cgg gtt tac tca gaa agc tac atc tcc agg cag acc agt gag act gta							1410
Arg Val Tyr Ser Glu Ser Tyr Ile Ser Arg Gln Thr Ser Glu Thr Val							
	345		350		355		
gaa aat gac aac gca tcg tcc ttt acc atg taa cacgagagca caaagcagca							1463
Glu Asn Asp Asn Ala Ser Ser Phe Thr Met							
	360		365				
tgccccgaaa gcctttgtga aacttgctat tacatgtga							1502

<210> 14
 <211> 366
 <212> PRT
 <213> Rattus norvegicus

<400> 14
 Met Asn Phe Thr Glu Ala Asn Tyr Gly Met Glu Asp Tyr Thr Gly Ser
 1 5 10 15
 Asp Tyr Ser Met Phe Pro Glu Thr Glu Pro Cys Ser Leu Gln Glu Val
 20 25 30
 Arg Asp Phe Thr Lys Val Phe Val Pro Ile Ala Tyr Ser Leu Ile Cys
 35 40 45
 Val Phe Gly Leu Leu Gly Asn Ile Met Val Val Ile Thr Phe Ala Phe
 50 55 60
 Tyr Lys Lys Ala Arg Ser Met Thr Asp Val Tyr Leu Leu Asn Met Ala
 65 70 75 80
 Ile Thr Asp Ile Leu Phe Val Leu Thr Leu Pro Phe Trp Ala Val Thr
 85 90 95
 His Ala Thr Asp Thr Trp Ile Phe Gly Asn Thr Met Cys Lys Leu Met
 100 105 110
 Lys Gly Thr Tyr Ala Val Asn Phe Asn Cys Gly Met Leu Leu Leu Ala
 115 120 125
 Cys Ile Ser Met Asp Arg Tyr Ile Ala Ile Val Gln Ala Thr Lys Ser
 130 135 140
 Phe Arg Val Arg Ser Arg Thr Leu Thr His Ser Lys Val Ile Cys Leu
 145 150 155 160
 Thr Val Trp Phe Val Ser Ile Ile Ile Ser Ser Pro Thr Phe Phe Phe
 165 170 175
 Asn Lys Gln Tyr Lys Leu Gln Gly Arg Asp Val Cys Glu Pro Gln Tyr
 180 185 190
 Lys Leu Val Ser Glu Pro Ile Thr Trp Lys Leu Leu Gly Met Gly Leu
 195 200 205
 Glu Leu Leu Phe Gly Phe Phe Ile Pro Leu Leu Phe Met Val Phe Cys

210		215		220
Tyr Leu Phe Ile Ile Lys Thr Leu Val Gln Ala Gln Asn Ser Lys Arg				
225		230		240
His Arg Ala Ile Arg Val Val Ile Ala Val Val Leu Val Phe Leu Ala				
	245		250	255
Cys Gln Ile Pro His Asn Met Val Leu Leu Val Thr Ala Ala Asn Thr				
	260		265	270
Gly Lys Met Gly Arg Ser Cys Ser Ala Glu Lys Ala Leu Ala Tyr Ala				
	275		280	285
Arg Asn Val Ala Glu Val Leu Ala Phe Leu His Cys Cys Leu Asn Pro				
	290		295	300
Val Leu Tyr Ala Phe Ile Gly Gln Lys Phe Arg Ser Tyr Phe Met Lys				
305		310		320
Ile Met Lys Asp Val Trp Cys Met Arg Arg Lys Ser Lys Val Pro Thr				
	325		330	335
Phe Phe Cys Ala Arg Val Tyr Ser Glu Ser Tyr Ile Ser Arg Gln Thr				
	340		345	350
Ser Glu Thr Val Glu Asn Asp Asn Ala Ser Ser Phe Thr Met				
	355		360	365

<210> 15
 <211> 1309
 <212> DNA
 <213> Rattus norvegicus (liver)

<220>
 <221> CDS
 <222> (150)..(1250)
 <223>

<400> 15	
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tctcacactt aggactggag cctggacaag cactaaggcg ggggtacctg gccagcccac	120
ttcggagctc agcgtttcct tgggaaacg atg aat ttc acc gag gcc aac tac	173
	Met Asn Phe Thr Glu Ala Asn Tyr
	1 5
gga atg gaa gat tat act ggc tca gat tac tct atg ttt cca gag acc	221
Gly Met Glu Asp Tyr Thr Gly Ser Asp Tyr Ser Met Phe Pro Glu Thr	
	10 15 20
gag cca tgc tct ctg caa gag gtc aga gac ttc acc aag gtg ttc gtg	269
Glu Pro Cys Ser Leu Gln Glu Val Arg Asp Phe Thr Lys Val Phe Val	
	25 30 35 40
cca atc gcc tac tcc tta atc tgt gtc ttt ggc ctc ctt ggc aat att	317
Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu Leu Gly Asn Ile	
	45 50 55
atg gtg gtg ata acc ttt gcc ttc tac aag aaa gcc agg tcc atg act	365
Met Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser Met Thr	
	60 65 70
gac gtc tac cta ttg aac atg gcc atc aca gac ata ctc ttt gtc ctc	413
Asp Val Tyr Leu Leu Asn Met Ala Ile Thr Asp Ile Leu Phe Val Leu	
	75 80 85
acc cta cca ttc tgg gca gtt act cat gcc act gac act tgg atc ttt	461
Thr Leu Pro Phe Trp Ala Val Thr His Ala Thr Asp Thr Trp Ile Phe	
	90 95 100
ggc aac acg atg tgt aaa ctg atg aaa ggc acg tat gcg gtc aac ttt	509
Gly Asn Thr Met Cys Lys Leu Met Lys Gly Thr Tyr Ala Val Asn Phe	
	105 110 115 120

aac tgt ggg atg ctg ctc ctg gcc tgt atc agc atg gac cgg tac att	557
Asn Cys Gly Met Leu Leu Leu Ala Cys Ile Ser Met Asp Arg Tyr Ile	
125 130 135	
gcc atc gtc cag gcg acc aaa tct ttc cgg gta cgc tcc aga aca ctg	605
Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Val Arg Ser Arg Thr Leu	
140 145 150	
acg cac agt aag gtc atc tgt ctg acg gtg tgg ttc gtt tcc atc atc	653
Thr His Ser Lys Val Ile Cys Leu Thr Val Trp Phe Val Ser Ile Ile	
155 160 165	
atc tca agc ccc aca ttc ttc ttc aac aag caa tac aag ctg cag ggc	701
Ile Ser Ser Pro Thr Phe Phe Phe Asn Lys Gln Tyr Lys Leu Gln Gly	
170 175 180	
cgt gat gtc tgc gag cct cag tac aag ctc gtc tcg gag ccc atc acg	749
Arg Asp Val Cys Glu Pro Gln Tyr Lys Leu Val Ser Glu Pro Ile Thr	
185 190 195 200	
tgg aaa ctg ctg ggc atg gga ctc gag ctg ctc ttt ggc ttc ttc atc	797
Trp Lys Leu Leu Gly Met Gly Leu Glu Leu Leu Phe Gly Phe Phe Ile	
205 210 215	
cct ttg ctg ttt atg gtg ttc tgt tac ctg ttc atc atc aag acc ttg	845
Pro Leu Leu Phe Met Val Phe Cys Tyr Leu Phe Ile Ile Lys Thr Leu	
220 225 230	
gtg cag gcc cag aat tcc aag agg cac aga gcc atc cga gtc gtg att	893
Val Gln Ala Gln Asn Ser Lys Arg His Arg Ala Ile Arg Val Val Ile	
235 240 245	
gct gtg gtt ctc gtg ttc ctg gct tgt cag atc cct cac aac atg gtc	941
Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro His Asn Met Val	
250 255 260	
ctc ctc gtg act gca gcc aac acg ggc aaa atg ggc cgc agc tgc agc	989
Leu Leu Val Thr Ala Ala Asn Thr Gly Lys Met Gly Arg Ser Cys Ser	
265 270 275 280	
gcc gag aaa gcc ctc gcc tac gcc agg aat gtg gct gag gtc ctg gct	1037
Ala Glu Lys Ala Leu Ala Tyr Ala Arg Asn Val Ala Glu Val Leu Ala	
285 290 295	
ttc ctg cac tgc tgt ctc aac ccc gtg ttg tat gcc ttc att gga cag	1085
Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile Gly Gln	
300 305 310	
aaa ttc aga agc tac ttc atg aag atc atg aag gat gtg tgg tgt atg	1133
Lys Phe Arg Ser Tyr Phe Met Lys Ile Met Lys Asp Val Trp Cys Met	
315 320 325	
agg agg aag agc aag gtg cct acc ttc ttc tgt gcc cgg gtt tac tca	1181
Arg Arg Lys Ser Lys Val Pro Thr Phe Phe Cys Ala Arg Val Tyr Ser	
330 335 340	
gaa agc tac atc tcc agg cag acc agt gag act gta gaa aat gac aac	1229
Glu Ser Tyr Ile Ser Arg Gln Thr Ser Glu Thr Val Glu Asn Asp Asn	
345 350 355 360	
gca tcg tcc ttt acc atg taa cacgagagca caaagcagca tgccccgaaa	1280
Ala Ser Ser Phe Thr Met	
365	
gcctttgtga aacttgctat tacatgtga	1309

<210> 16

<211> 25

<212> DNA

<213> Artificial

<220>

<223> Oligonucleotide designed to act as primer for amplifying CCR6

cDNA derived from rat kidney.

<400> 16
tgtattgaag acagaacact tgtgg 25

<210> 17
<211> 28
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as primer for amplifying CCR6
cDNA derived from rat kidney or rat liver.

<400> 17
tcacatgtaa tagcaagttt caciaaagg 28

<210> 18
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as primer for amplifying CCR6
cDNA derived from rat liver.

<400> 18
gcattctcact acccgctctct c 21

<210> 19
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as primer for amplifying fragment
of rat CCR6 gene transcript.

<400> 19
ggacgatgcg ttgtcatttt c 21

<210> 20
<211> 22
<212> DNA
<213> Artificial

<220>
<223> Oligonucleotide designed to act as primer for amplifying fragment
of rat CCR6 gene transcript.

<400> 20
ccgcagctgc agcgccgaga aa 22

<210> 21
<211> 20
<212> DNA
<213> Artificial

<220>

<223> Oligonucleotide designed to act as primer for amplifying fragment
of rat CCR6 gene transcript.

<400> 21

gtgcccgggt ttactcagaa

20